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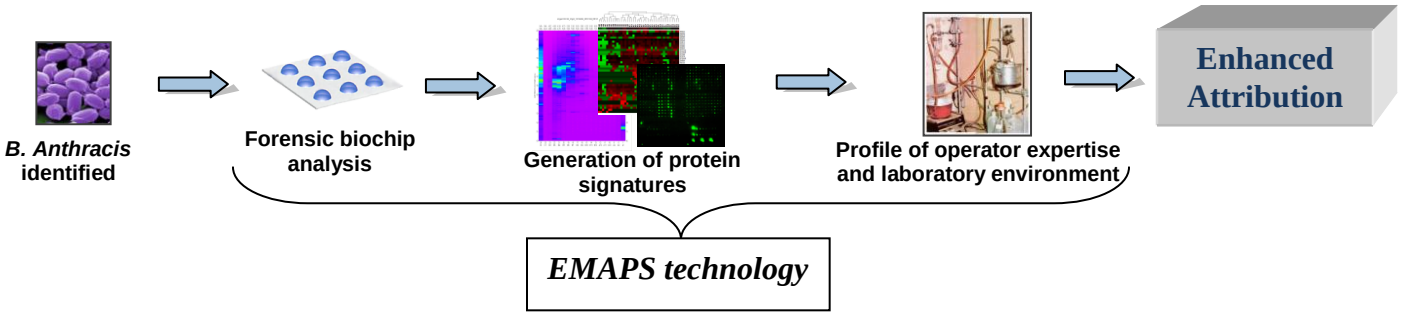
National Security

Enhanced Molecular Attribution through Proteomic Signatures (EMAPS)



There is a critical need for methodologies that generate a detailed signature of a biothreat agent (BTA). Genetic analysis alone cannot provide a full description of a BTA; information on how the material was prepared, by whom and the resources available to the operator cannot be obtained by genetic means. Therefore, information useful for attribution will require novel methods that are orthogonal to genetic analysis. To be useful, these methods must provide a signature of the BTA that is highly sensitive and detailed enough for attribution. In some scenarios, the signature must be sufficiently reliable to withstand legal challenges in court. The most appropriate source of molecular signatures for this task is the proteome.

We have developed a novel forensic methodology specific to BTA attribution, **Enhanced Molecular Attribution through Proteomic Signatures** (**EMAPS**). *Bacillus anthracis* spores are the model organism for the validation of the methodology because they are among the BTAs most likely to be used as a weapon. This is for at least two reasons: 1) *B. anthracis* is easy to generate in a form that stores well and readily disperses and 2) The disease caused by *B. anthracis*, anthrax, is usually fatal.

Our approach quantitatively analyzes the molecular composition of the protective protein shells (the coat and exosporium) encasing *B. anthracis* spores. The composition of these shells varies greatly with the *B. anthracis* strain and, critically, with the spore preparation method. As a result, the EMAPS technology can discriminate among *B. anthracis* and other Bacillus strains and, most importantly, provide detailed information regarding the methods used to culture, purify and store the spores. Therefore, the EMAPS technology can help identify not only the specific organism used, but also the facilities used in its preparation and the technical sophistication of the operator.

Our approach is both innovative and a major improvement on previous spore analytic methods because of the chosen molecular separation and protein chip fabrication technologies and the manner in which they are integrated into a single system. Our methodology is particularly well suited for the security mission because it combines sensitivity with a highly robust, semi-automated platform that does not require a specialized laboratory or expensive mass spectral analysis.

A multidisciplinary team, drawing from laboratories in the USG, industry and academia, is ideally positioned to address this complex problem in attribution.

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